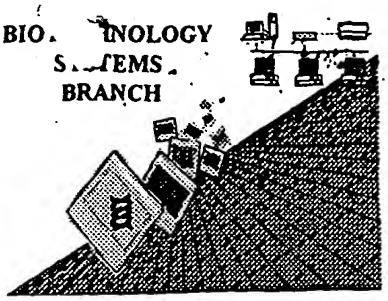

RAW SEQUENCE LISTING ERROR REPORT

#12

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: US 09/479,608

Source: OIPE

Date Processed by STIC: 08 09 2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/479,608

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTW

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11	✓ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/479,608

DATE: 08/09/2001
TIME: 13:18:12

Input Set : A:\35918.txt
Output Set: N:\CRF3\08092001\I479608.raw

Does Not Comply
Corrected Diskette Needed

<110> APPLICANT: Drmanac, R.
Drmanac, S.
Kita, D.
Cooke, C.
Xu, C.
<120> TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
<130> FILE REFERENCE: 28110/35918
<140> CURRENT APPLICATION NUMBER: US 09/479,608
<141> CURRENT FILING DATE: 2000-01-06
<150> PRIOR APPLICATION NUMBER: US 60/115,284
<151> PRIOR FILING DATE: 1999-01-06
<160> NUMBER OF SEQ ID NOS: 71
<170> SOFTWARE: PatentIn version 3.0
<210> SEQ ID NO: 1
<211> LENGTH: 10
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description required in field 223
<400> SEQUENCE: 1
aaaaaaaaaa 10
<210> SEQ ID NO: 2
<211> LENGTH: 10
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of artificial sequence required
<400> SEQUENCE: 2
acacacacac 10
<210> SEQ ID NO: 3
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: description of artificial sequence required
<400> SEQUENCE: 3
atctgtgtct gaagtagtcc 20
<210> SEQ ID NO: 4
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION:
<400> SEQUENCE: 4
atctctggct gaagtagtcc 20
<210> SEQ ID NO: 5
<211> LENGTH: 43

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence
75 <220> FEATURE:
76 <221> NAME/KEY: misc_feature
77 <222> LOCATION:
78 <223> OTHER INFORMATION: b = C or G or T OK
80 <400> SEQUENCE: 5
81 bbbbbbattt cbbbbbgcac tbbbbgtttg bbbacacgbb bbb 43
83 <210> SEQ ID NO: 6
84 <211> LENGTH: 43
85 <212> TYPE: DNA
86 <213> ORGANISM: Artificial Sequence — Field 223 with description of artificial sequence required
88 <220> FEATURE:
89 <221> NAME/KEY: misc_feature
90 <222> LOCATION:
91 <223> OTHER INFORMATION: b = C or G or T
93 <400> SEQUENCE: 6
94 bbbbbbattt gbbbacactb bbbgtttcbb bbbgcacgbb bbb 43
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 10
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION:
104 <400> SEQUENCE: 7
105 ggtctcccca 10
107 <210> SEQ ID NO: 8
108 <211> LENGTH: 10
109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial Sequence
112 <220> FEATURE:
113 <223> OTHER INFORMATION:
115 <400> SEQUENCE: 8
116 gtctccccaa 10
118 <210> SEQ ID NO: 9
119 <211> LENGTH: 10
120 <212> TYPE: DNA
121 <213> ORGANISM: Artificial Sequence
124 <220> FEATURE:
125 <223> OTHER INFORMATION:
127 <400> SEQUENCE: 9
128 tctccccaag 10
130 <210> SEQ ID NO: 10
131 <211> LENGTH: 10
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
135 <220> FEATURE:
136 <223> OTHER INFORMATION:
138 <400> SEQUENCE: 10

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143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
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150 tccccaaggc                                                          10
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155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION:
160 <400> SEQUENCE: 12
161 ccccaaggcg                                                          10
163 <210> SEQ ID NO: 13
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165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
168 <220> FEATURE:
169 <223> OTHER INFORMATION:
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177 <213> ORGANISM: Artificial Sequence
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187 <212> TYPE: DNA
188 <213> ORGANISM: Artificial Sequence
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198 <211> LENGTH: 30
199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION:
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206 tgcttgccac aggtctcccc aaggcgcact                                     30
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Field 223 description required

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212 <213> ORGANISM: Artificial Sequence
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217 <400> SEQUENCE: 17
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221 <210> SEQ ID NO: 18
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223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
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227 <223> OTHER INFORMATION:
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233 <210> SEQ ID NO: 19
234 <211> LENGTH: 10
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION:
241 <400> SEQUENCE: 19
242 gtctccccaa 10
244 <210> SEQ ID NO: 20
245 <211> LENGTH: 10
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
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253 tctccccaag 10
255 <210> SEQ ID NO: 21
256 <211> LENGTH: 10
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION:
263 <400> SEQUENCE: 21
264 ctccccaagg 10
266 <210> SEQ ID NO: 22
267 <211> LENGTH: 10
268 <212> TYPE: DNA
269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:
272 <223> OTHER INFORMATION:
274 <400> SEQUENCE: 22
275 tccccaaggc 10
277 <210> SEQ ID NO: 23

278 <211> LENGTH: 10
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION:
285 <400> SEQUENCE: 23
286 ccccaaggcg 10
288 <210> SEQ ID NO: 24
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290 <212> TYPE: DNA
291 <213> ORGANISM: Artificial Sequence
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299 <210> SEQ ID NO: 25
300 <211> LENGTH: 10
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequences
304 <220> FEATURE:
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308 <400> SEQUENCE: 25
309 ccaaggcgca 10
311 <210> SEQ ID NO: 26
312 <211> LENGTH: 10
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial Sequence
316 <220> FEATURE:
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323 <211> LENGTH: 10
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial Sequence
327 <220> FEATURE:
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330 <400> SEQUENCE: 27
331 caggtctccc 10
333 <210> SEQ ID NO: 28
334 <211> LENGTH: 10
335 <212> TYPE: DNA
336 <213> ORGANISM: Artificial Sequences
338 <220> FEATURE:
339 <223> OTHER INFORMATION:
341 <400> SEQUENCE: 28
342 gcttgccaca 10
344 <210> SEQ ID NO: 29
345 <211> LENGTH: 10

VERIFICATION SUMMARY DATE: 08/09/2001
PATENT APPLICATION: US/09/479,608 TIME: 13:18:13

Input Set : A:\35918.txt
Output Set: N:\CRF3\08092001\I479608.raw

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821-1.825. Applicant's attention is directed to these regulations, published at 114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

☐ 7. Other: _____

Applicant must provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact

For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.